10/019065

SEQUENCE LISTING

<170> PatentIn Ver. 2.0

<210> 1
<211> 208
<212> PRT
<213> human

<400> 1

```
Gln Val His Gly Gly Phe Ser Gln Trp Ser Ala Trp Arg Ala Cys Ser
  1               5                  10                  15

Val Thr Cys Gly Lys Gly Ile Gln Lys Arg Ser Arg Leu Cys Asn Gln
             20                  25                  30

Pro Leu Pro Ala Asn Gly Gly Lys Pro Cys Gln Gly Ser Asp Leu Glu
         35                  40                  45

Met Arg Asn Cys Gln Asn Lys Pro Cys Pro Val Asp Gly Ser Trp Ser
     50                  55                  60

Glu Trp Ser Leu Trp Glu Glu Cys Thr Arg Ser Cys Gly Arg Gly Asn
 65                  70                  75                  80

Gln Thr Arg Thr Arg Thr Cys Asn Asn Pro Ser Val Gln His Gly Gly
                 85                  90                  95

Arg Pro Cys Glu Gly Asn Ala Val Glu Ile Ile Met Cys Asn Ile Arg
            100                 105                 110

Pro Cys Pro Val His Gly Ala Trp Ser Ala Trp Gln Pro Trp Gly Thr
        115                 120                 125

Cys Ser Glu Ser Cys Gly Lys Gly Thr Gln Thr Arg Ala Arg Leu Cys
    130                 135                 140

Asn Asn Pro Pro Pro Ala Phe Gly Gly Ser Tyr Cys Asp Gly Ala Glu
145                 150                 155                 160

Thr Gln Met Gln Val Cys Asn Glu Arg Asn Cys Pro Ile His Gly Lys
                165                 170                 175

Trp Ala Thr Trp Ala Ser Trp Ser Ala Cys Ser Val Ser Cys Gly Gly
            180                 185                 190

Gly Ala Arg Gln Arg Thr Arg Gly Cys Ser Asp Pro Val Pro Gln Tyr
        195                 200                 205
```

<210> 2
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Random sequence

<400> 2
Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Ala Asn Pro Gln Leu
1 5 10 15

Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu
20 25 30

Arg Asp Asn Gln Leu Val Val Glu Gly Leu Tyr Leu Ile Tyr Ser Gln
35 40 45

Val Leu Phe
50

<210> 3
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Random sequence

<400> 3
Arg Ala Pro Phe Lys Lys Ser Trp Ala Tyr Leu Gln Val Ala Lys His
1 5 10 15

Lys Leu Ser Trp Asn Lys Asp Gly Ile Leu His Gly Val Arg Tyr Gln
20 25 30

Asp Gly Asn Leu Val Ile Gln Phe Pro Gly Leu Tyr Phe Ile Ile Cys
35 40 45

Gln Leu Gln Phe
50

<210> 4
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:FLAG sequence
for expressed protein purification

<400> 4
Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 5
<211> 6
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:sequence with antineoangiogenic activity

<400> 5
Cys Ser Val Thr Cys Gly
1 5

<210> 6
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:isolated type 1 thrombospondin domain sequence

<400> 6
Asp Gly Trp Ser Pro Trp Ser Glu Trp Thr Ser Cys Ser Thr Ser Cys
1 5 10 15

Gly Asn Gly Ile Gln Gln Arg Gly Arg Ser Cys Asp Ser Leu Asn Asn
20 25 30

Arg Cys Glu Gly Ser Ser Val Gln Thr Arg Thr Cys His Ile Gln Glu
35 40 45

Cys Asp
50

<210> 7
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:isolated type 1 thrombospondin domain sequence

<400> 7
Gly Gly Trp Ser His Trp Ser Pro Trp Ser Ser Cys Ser Val Thr Cys
1 5 10 15

Gly Asp Gly Val Ile Thr Arg Ile Arg Leu Cys Asn Ser Pro Ser Pro
20 25 30

Gln Met Asn Gly Lys Pro Cys Glu Gly Glu Ala Arg Glu Thr Lys Ala
35 40 45

Cys Lys Lys Asp Ala Cys Pro
50 55

<210> 8
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:isolated type 1 thrombospondin domain sequence

<400> 8
Gly Gly Trp Gly Pro Trp Ser Pro Trp Asp Ile Cys Ser Val Thr Cys
1 5 10 15

Gly Gly Gly Val Gln Lys Arg Ser Arg Leu Cys Asn Asn Pro Thr Pro
20 25 30

Gln Phe Gly Gly Lys Asp Cys Val Gly Asp Val Thr Glu Asn Gln Ile
35 40 45

Cys Asn Lys Gln Asp Cys Pro
50 55

<210> 9
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:isolated type 1 thrombospondin domain sequence

<400> 9
Glu Gly Trp Ser Pro Trp Ala Glu Trp Thr Gln Cys Ser Val Thr Cys
1 5 10 15

Gly Ser Gly Thr Gln Gln Arg Gly Arg Ser Cys Asp Val Thr Ser Asn
20 25 30

Thr Cys Leu Gly Pro Ser Ile Gln Thr Arg Ala Cys Ser Leu Ser Lys
35 40 45

Cys Asp
50

<210> 10
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:isolated type 1 thrombospondin domain sequence

<400> 10
Gly Gly Trp Ser His Trp Ser Pro Trp Ser Ser Cys Ser Val Thr Cys
1 5 10 15

Gly Val Gly Asn Ile Thr Arg Ile Arg Leu Cys Asn Ser Pro Val Pro
20 25 30

Gln Met Gly Gly Lys Asn Cys Lys Gly Ser Gly Arg Glu Thr Lys Ala
35 40 45

Cys Gln Gly Ala Pro Cys Pro
50 55

<210> 11
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:isolated type 1 thrombospondin domain sequence

<400> 11
Gly Arg Trp Ser Pro Trp Ser Pro Trp Ser Ala Cys Thr Val Thr Cys
1 5 10 15

Ala Gly Gly Ile Arg Glu Arg Thr Arg Val Cys Asn Ser Pro Glu Pro
20 25 30

Gln Tyr Gly Gly Lys Ala Cys Val Gly Asp Val Gln Glu Arg Gln Met
35 40 45

Cys Asn Lys Arg Ser Cys Pro
50 55

<210> 12
<211> 54
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:isolated type 1 thrombospondin domain sequence

<400> 12
Gly Gly Trp Lys Leu Trp Ser Leu Trp Gly Glu Cys Thr Arg Asp Cys
1 5 10 15

Gly Gly Gly Leu Gln Thr Arg Thr Arg Thr Cys Leu Pro Ala Pro Gly
20 25 30

Val Glu Gly Gly Gly Cys Glu Gly Val Leu Glu Glu Gly Arg Gln Cys
35 40 45

Asn Arg Glu Ala Cys Gly
50

<210> 13
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:isolated type 1 thrombospondin domain sequence

<400> 13
Pro Ala Ala Glu Glu Trp Ser Pro Trp Ser Val Cys Ser Ser Thr Cys
1 5 10 15

Gly Glu Gly Trp Gln Thr Arg Thr Arg Phe Cys Val Ser Ser Ser Tyr
20 25 30

Ser Thr Gln Cys Ser Gly Pro Leu Arg Glu Gln Arg Leu Cys Asn Asn
35 40 45

Ser Ala Val Cys Pro
50

<210> 14
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:isolated type 1 thrombospondin domain sequence

<400> 14
Gly Ala Trp Asp Glu Trp Ser Pro Trp Ser Leu Cys Ser Ser Thr Cys
1 5 10 15

Gly Arg Gly Phe Arg Asp Arg Thr Arg Thr Cys Arg Pro Pro Gln Phe
20 25 30

Gly Gly Asn Pro Cys Glu Gly Pro Glu Lys Gln Thr Lys Phe Cys Asn
35 40 45

Ile Ala Leu Cys Pro
50

<210> 15
<211> 53
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:isolated type 1 thrombospondin domain sequence

<400> 15
Gly Asn Trp Asn Glu Trp Ser Ser Trp Ser Ala Cys Ser Ala Ser Cys
1 5 10 15

Ser Gln Gly Arg Gln Gln Arg Thr Arg Glu Cys Asn Gly Pro Ser Tyr
20 25 30

Gly Gly Ala Glu Cys Gln Gly His Trp Val Glu Thr Arg Asp Cys Phe
35 40 45

Leu Gln Gln Cys Pro
50

<210> 16
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:isolated type 1 thrombospondin domain sequence

<400> 16
Gly Lys Trp Gln Ala Trp Ala Ser Trp Gly Ser Cys Ser Val Thr Cys
1 5 10 15

Gly Ala Gly Ser Gln Arg Arg Glu Arg Val Cys Ser Gly Pro Phe Phe
20 25 30

Gly Gly Ala Ala Cys Gln Gly Pro Gln Asp Glu Tyr Arg Gln Cys Gly
35 40 45

Thr Gln Arg Cys Pro
50

<210> 17
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:isolated type 1 thrombospondin domain sequence

<400> 17
Pro Ala Ala Glu Glu Trp Ser Pro Trp Ser Val Cys Ser Leu Thr Cys
1 5 10 15

Gly Gln Gly Leu Gln Val Arg Thr Arg Ser Cys Val Ser Ser Pro Tyr
20 25 30

Gly Thr Leu Cys Ser Gly Pro Leu Arg Glu Thr Arg Pro Cys Asn Asn
35 40 45

Ser Ala Thr Cys Pro
50

<210> 18
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:isolated type 1 thrombospondin domain sequence

<400> 18
Gly Val Trp Glu Glu Trp Gly Ser Trp Ser Leu Cys Ser Arg Ser Cys
1 5 10 15

Gly Arg Gly Ser Arg Ser Arg Met Arg Thr Cys Val Pro Pro Gln His
20 25 30

Gly Gly Lys Ala Cys Glu Gly Pro Glu Leu Gln Thr Lys Leu Cys Ser
35 40 45

Met Ala Ala Cys Pro
50

<210> 19
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:isolated type 1 thrombospondin domain sequence

<400> 19
Gly Gln Trp Leu Glu Trp Gly Pro Trp Gly Pro Cys Ser Thr Ser Cys
1 5 10 15

Ala Asn Gly Thr Gln Gln Arg Ser Arg Lys Cys Ser Val Ala Gly Pro
20 25 30

Ala Trp Ala Thr Cys Thr Gly Ala Leu Thr Asp Thr Arg Glu Cys Ser
35 40 45

Asn Leu Glu Cys Pro
50

<210> 20
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:isolated type 1
thrombospondin domain sequence

<400> 20
Ser Lys Trp Gly Pro Trp Asn Ala Trp Ser Leu Cys Ser Lys Thr Cys
1 5 10 15

Asp Thr Gly Trp Gln Arg Arg Phe Arg Met Cys Gln Ala Thr Gly Thr
20 25 30

Gln Gly Tyr Pro Cys Glu Gly Thr Gly Glu Glu Val Lys Pro Cys Ser
35 40 45

Glu Lys Arg Cys Pro
50

<210> 21
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:isolated type 1
thrombospondin domain sequence

<400> 21
Ser Gly Val Glu Glu Trp Ser Gln Trp Ser Thr Cys Ser Val Thr Cys
1 5 10 15

Gly Gln Gly Ser Gln Val Arg Thr Arg Thr Cys Val Ser Pro Tyr Gly
20 25 30

Thr His Cys Ser Gly Pro Leu Arg Glu Ser Arg Val Cys Asn Asn Thr
35 40 45

Ala Leu Cys Pro
50

<210> 22
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:isolated type 1
thrombospondin domain sequence

<400> 22
Gly Val Trp Glu Glu Trp Ser Pro Trp Ser Leu Cys Ser Phe Thr Cys
1 5 10 15

Gly Arg Gly Gln Arg Thr Arg Thr Arg Ser Cys Thr Pro Pro Gln Tyr
20 25 30

Gly Gly Arg Pro Cys Glu Gly Pro Glu Thr His His Lys Pro Cys Asn
35 40 45

Ile Ala Leu Cys Pro
50

<210> 23
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:isolated type 1 thrombospondin domain sequence

<400> 23
Gly Gln Trp Gln Glu Trp Ser Ser Trp Ser Gln Cys Ser Val Thr Cys
1 5 10 15

Ser Asn Gly Thr Gln Gln Arg Ser Arg Gln Cys Thr Ala Ala Ala His
20 25 30

Gly Gly Ser Glu Cys Arg Gly Pro Trp Ala Glu Ser Arg Glu Cys Tyr
35 40 45

Asn Pro Glu Cys Thr
50

<210> 24
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:isolated type 1 thrombospondin domain sequence

<400> 24
Gly Gln Trp Asn Gln Trp Gly His Trp Ser Gly Cys Ser Lys Ser Cys
1 5 10 15

Asp Gly Gly Trp Glu Arg Arg Ile Arg Thr Cys Gln Gly Ala Val Ile
20 25 30

Thr Gly Gln Gln Cys Glu Gly Thr Gly Glu Glu Val Arg Arg Cys Ser
35 40 45

Glu Gln Arg Cys Pro
50

<210> 25
<211> 55
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:isolated type 1 thrombospondin domain sequence

<400> 25
Gly Gly Phe Ser Gln Trp Ser Ala Trp Arg Ala Cys Ser Val Thr Cys
1 5 10 15

Gly Lys Gly Ile Gln Lys Arg Ser Arg Leu Cys Asn Gln Pro Leu Pro
20 25 30

Ala Asn Gly Gly Lys Pro Cys Gln Gly Ser Asp Leu Glu Met Arg Asn
35 40 45

Cys Gln Asn Lys Pro Cys Pro
50 55

<210> 26
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:isolated type 1 thrombospondin domain sequence

<400> 26
Gly Ser Trp Ser Glu Trp Ser Leu Trp Glu Glu Cys Thr Arg Ser Cys
1 5 10 15

Gly Arg Gly Asn Gln Thr Arg Thr Arg Thr Cys Asn Asn Pro Ser Val
20 25 30

Gln His Gly Gly Arg Pro Cys Glu Gly Asn Ala Val Glu Ile Ile Met
35 40 45

Cys Asn Ile Arg Pro Cys Pro
50 55

<210> 27
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:isolated type 1 thrombospondin domain sequence

<400> 27
Gly Ala Trp Ser Ala Trp Gln Pro Trp Gly Thr Cys Ser Glu Ser Cys
1 5 10 15

Gly Lys Gly Thr Gln Thr Arg Ala Arg Leu Cys Asn Asn Pro Pro Pro
20 25 30

Ala Phe Gly Gly Ser Tyr Cys Asp Gly Ala Glu Thr Gln Met Gln Val
35 40 45

Cys Asn Glu Arg Asn Cys Pro
50 55

<210> 28
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:isolated type 1 thrombospondin domain sequence

<400> 28
Gly Lys Trp Ala Thr Trp Ala Ser Trp Ser Ala Cys Ser Val Ser Cys
1 5 10 15

Gly Gly Gly Ala Arg Gln Arg Thr Arg Gly Cys Ser Asp Pro Val Pro
20 25 30

Gln Tyr Gly Gly Arg Lys Cys Glu Gly Ser Asp Val Gln Ser Asp Phe
35 40 45

Cys Asn Ser Asp Pro Cys Pro
50 55

<210> 29
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:isolated type 1 thrombospondin domain sequence

<400> 29
Gly Asn Trp Ser Pro Trp Ser Gly Trp Gly Thr Cys Ser Arg Thr Cys
1 5 10 15

Asn Gly Gly Gln Met Arg Arg Tyr Arg Thr Cys Asp Asn Pro Pro Pro
20 25 30

Ser Asn Gly Gly Arg Ala Cys Gly Gly Pro Asp Ser Gln Ile Gln Arg
35 40 45

Cys Asn Thr Asp Met Cys Pro
50 55

<210> 30
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:isolated type 1 thrombospondin domain sequence

<400> 30
Gly Ser Trp Gly Ser Trp His Ser Trp Ser Gln Cys Ser Ala Ser Cys
1 5 10 15

Gly Gly Gly Glu Lys Thr Arg Lys Arg Leu Cys Asp His Pro Val Pro
20 25 30

Val Lys Gly Gly Arg Pro Cys Pro Gly Asp Thr Thr Gln Val Thr Arg
35 40 45

Cys Asn Val Gln Ala Cys Pro
50 55

<210> 31
<211> 197
<212> PRT
<213> human

<400> 31
Gln Trp Ser Ala Trp Arg Ala Cys Ser Val Thr Cys Gly Lys Gly Ile
1 5 10 15

Gln Lys Arg Ser Arg Leu Cys Asn Gln Pro Leu Pro Ala Asn Gly Gly
20 25 30

Lys Pro Cys Gln Gly Ser Asp Leu Glu Met Arg Asn Cys Gln Asn Lys
35 40 45

Pro Cys Pro Val Asp Gly Ser Trp Ser Glu Trp Ser Leu Trp Glu Glu
50 55 60

Cys Thr Arg Ser Cys Gly Arg Gly Asn Gln Thr Arg Thr Arg Thr Cys
65 70 75 80

Asn Asn Pro Ser Val Gln His Gly Gly Arg Pro Cys Glu Gly Asn Ala
85 90 95

Val Glu Ile Ile Met Cys Asn Ile Arg Pro Cys Pro Val His Gly Ala
100 105 110

Trp Ser Ala Trp Gln Pro Trp Gly Thr Cys Ser Glu Ser Cys Gly Lys
115 120 125

Gly Thr Gln Thr Arg Ala Arg Leu Cys Asn Asn Pro Pro Pro Ala Phe
130 135 140

```
Gly Gly Ser Tyr Cys Asp Gly Ala Glu Thr Gln Met Gln Val Cys Asn
145                 150                 155                 160

Glu Arg Asn Cys Pro Ile His Gly Lys Trp Ala Thr Trp Ala Ser Trp
                165                 170                 175

Ser Ala Cys Ser Val Ser Cys Gly Gly Gly Ala Arg Gln Arg Thr Arg
            180                 185                 190

Gly Cys Ser Asp Pro
        195
```

<210> 32
<211> 194
<212> PRT
<213> human

<400> 32

```
Glu Trp Ser Pro Trp Ser Val Cys Ser Ser Thr Cys Gly Glu Gly Trp
  1               5                  10                  15

Gln Thr Arg Thr Arg Phe Cys Val Ser Ser Ser Tyr Ser Thr Gln Cys
            20                  25                  30

Ser Gly Pro Leu Arg Glu Gln Arg Leu Cys Asn Asn Ser Ala Val Cys
        35                  40                  45

Pro Val His Gly Ala Trp Asp Glu Trp Ser Pro Trp Ser Leu Cys Ser
    50                  55                  60

Ser Thr Cys Gly Arg Gly Phe Arg Asp Arg Thr Arg Thr Cys Arg Pro
65                  70                  75                  80

Pro Gln Phe Gly Gly Asn Pro Cys Glu Gly Pro Glu Lys Gln Thr Lys
                85                  90                  95

Phe Cys Asn Ile Ala Leu Cys Pro Gly Arg Ala Val Asp Gly Asn Trp
            100                 105                 110

Asn Glu Trp Ser Ser Trp Ser Ala Cys Ser Ala Ser Cys Ser Gln Gly
        115                 120                 125

Arg Gln Gln Arg Thr Arg Glu Cys Asn Gly Pro Ser Tyr Gly Gly Ala
    130                 135                 140

Glu Cys Gln Gly His Trp Val Glu Thr Arg Asp Cys Phe Leu Gln Gln
145                 150                 155                 160

Cys Pro Val Asp Gly Lys Trp Gln Ala Trp Ala Ser Trp Gly Ser Cys
                165                 170                 175

Ser Val Thr Cys Gly Ala Gly Ser Gln Arg Arg Glu Arg Val Cys Ser
            180                 185                 190

Gly Pro
```

<210> 33
<211> 1335
<212> PRT
<213> human

<400> 33
Thr Pro Ile Gly Arg Pro Arg Ile Arg His Gln Asp Lys Arg Thr Val
1 5 10 15

Asp Leu Thr Val Gln Val Pro Pro Ser Ile Ala Asp Glu Pro Thr Asp
20 25 30

Phe Leu Val Thr Lys His Ala Pro Ala Val Ile Thr Cys Thr Ala Ser
35 40 45

Gly Val Pro Phe Pro Ser Ile His Trp Thr Lys Asn Gly Ile Arg Leu
50 55 60

Leu Pro Arg Gly Asp Gly Tyr Arg Ile Leu Ser Ser Gly Ala Ile Glu
65 70 75 80

Ile Leu Ala Thr Gln Leu Asn His Ala Gly Arg Tyr Thr Cys Val Ala
85 90 95

Arg Asn Ala Ala Gly Ser Ala His Arg His Val Thr Leu His Val His
100 105 110

Glu Pro Pro Val Ile Gln Pro Gln Pro Ser Glu Leu His Val Ile Leu
115 120 125

Asn Asn Pro Ile Leu Leu Pro Cys Glu Ala Thr Gly Thr Pro Ser Pro
130 135 140

Phe Ile Thr Trp Gln Lys Glu Gly Ile Asn Val Asn Thr Ser Gly Arg
145 150 155 160

Asn His Ala Val Leu Pro Ser Gly Gly Leu Gln Ile Ser Arg Ala Val
165 170 175

Arg Glu Asp Ala Gly Thr Tyr Met Cys Val Ala Gln Asn Pro Ala Gly
180 185 190

Thr Ala Leu Gly Lys Ile Lys Leu Asn Val Gln Val Pro Pro Val Ile
195 200 205

Ser Pro His Leu Lys Glu Tyr Val Ile Ala Val Asp Lys Pro Ile Thr
210 215 220

Leu Ser Cys Glu Ala Asp Gly Leu Pro Pro Pro Asp Ile Thr Trp His
225 230 235 240

Lys Asp Gly Arg Ala Ile Val Glu Ser Ile Arg Gln Arg Val Leu Ser
245 250 255

```
Ser Gly Ser Leu Gln Ile Ala Phe Val Gln Pro Gly Asp Ala Gly His
            260                 265                 270

Tyr Thr Cys Met Ala Ala Asn Val Ala Gly Ser Ser Ser Thr Ser Thr
        275                 280                 285

Lys Leu Thr Val His Val Pro Pro Arg Ile Arg Ser Thr Lys Gly His
    290                 295                 300

Tyr Thr Val Asn Glu Asn Ser Gln Ala Ile Leu Pro Cys Val Ala Asp
305                 310                 315                 320

Gly Ile Pro Thr Pro Ala Ile Asn Trp Lys Lys Asp Asn Val Leu Leu
                325                 330                 335

Ala Asn Leu Leu Gly Lys Tyr Thr Ala Glu Pro Tyr Gly Glu Leu Ile
            340                 345                 350

Leu Glu Asn Val Val Leu Glu Asp Ser Gly Phe Tyr Thr Cys Val Ala
        355                 360                 365

Asn Asn Ala Ala Gly Glu Asp Thr His Thr Val Ser Leu Thr Val His
    370                 375                 380

Val Leu Pro Thr Phe Thr Glu Leu Pro Gly Asp Val Ser Leu Asn Lys
385                 390                 395                 400

Gly Glu Gln Leu Arg Leu Ser Cys Lys Ala Thr Gly Ile Pro Leu Pro
                405                 410                 415

Lys Leu Thr Trp Thr Phe Asn Asn Asn Ile Ile Pro Ala His Phe Asp
            420                 425                 430

Ser Val Asn Gly His Ser Glu Leu Val Ile Glu Arg Val Ser Lys Glu
        435                 440                 445

Asp Ser Gly Thr Tyr Val Cys Thr Ala Glu Asn Ser Val Gly Phe Val
    450                 455                 460

Lys Ala Ile Gly Phe Val Tyr Val Lys Glu Pro Pro Val Phe Lys Gly
465                 470                 475                 480

Asp Tyr Pro Ser Asn Trp Ile Glu Pro Leu Gly Gly Asn Ala Ile Leu
                485                 490                 495

Asn Cys Glu Val Lys Gly Asp Pro Thr Pro Thr Ile Gln Trp Asn Arg
            500                 505                 510

Lys Gly Val Asp Ile Glu Ile Ser His Arg Ile Arg Gln Leu Gly Asn
        515                 520                 525

Gly Ser Leu Ala Ile Tyr Gly Thr Val Asn Glu Asp Ala Gly Asp Tyr
    530                 535                 540

Thr Cys Val Ala Thr Asn Glu Ala Gly Val Val Glu Arg Ser Met Ser
545                 550                 555                 560
```

Leu Thr Leu Arg Ser Pro Pro Ile Ile Thr Leu Glu Pro Val Glu Thr
565 570 575

Val Ile Asn Ala Gly Gly Lys Ile Ile Leu Asn Cys Gln Ala Thr Gly
580 585 590

Glu Pro Gln Pro Thr Ile Thr Trp Ser Arg Gln Gly His Ser Ile Ser
595 600 605

Trp Asp Asp Arg Val Asn Val Leu Ser Asn Asn Ser Leu Tyr Ile Ala
610 615 620

Asp Ala Gln Lys Glu Asp Thr Ser Glu Phe Glu Cys Val Ala Arg Asn
625 630 635 640

Leu Met Gly Ser Val Leu Val Arg Val Pro Val Ile Val Gln Val His
645 650 655

Gly Gly Phe Ser Gln Trp Ser Ala Trp Arg Ala Cys Ser Val Thr Cys
660 665 670

Gly Lys Gly Ile Gln Lys Arg Ser Arg Leu Cys Asn Gln Pro Leu Pro
675 680 685

Ala Asn Gly Gly Lys Pro Cys Gln Gly Ser Asp Leu Glu Met Arg Asn
690 695 700

Cys Gln Asn Lys Pro Cys Pro Val Asp Gly Ser Trp Ser Glu Trp Ser
705 710 715 720

Leu Trp Glu Glu Cys Thr Arg Ser Cys Gly Arg Gly Asn Gln Thr Arg
725 730 735

Thr Arg Thr Cys Asn Asn Pro Ser Val Gln His Gly Gly Arg Pro Cys
740 745 750

Glu Gly Asn Ala Val Glu Ile Ile Met Cys Asn Ile Arg Pro Cys Pro
755 760 765

Val His Gly Ala Trp Ser Ala Trp Gln Pro Trp Gly Thr Cys Ser Glu
770 775 780

Ser Cys Gly Lys Gly Thr Gln Thr Arg Ala Arg Leu Cys Asn Asn Pro
785 790 795 800

Pro Pro Ala Phe Gly Gly Ser Tyr Cys Asp Gly Ala Glu Thr Gln Met
805 810 815

Gln Val Cys Asn Glu Arg Asn Cys Pro Ile His Gly Lys Trp Ala Thr
820 825 830

Trp Ala Ser Trp Ser Ala Cys Ser Val Ser Cys Gly Gly Gly Ala Arg
835 840 845

Gln Arg Thr Arg Gly Cys Ser Asp Pro Val Pro Gln Tyr Gly Gly Arg
850 855 860

```
Lys Cys Glu Gly Ser Asp Val Gln Ser Asp Phe Cys Asn Ser Asp Pro
865                 870                 875                 880

Cys Pro Thr His Gly Asn Trp Ser Pro Trp Ser Gly Trp Gly Thr Cys
                885                 890                 895

Ser Arg Thr Cys Asn Gly Gly Gln Met Arg Arg Tyr Arg Thr Cys Asp
            900                 905                 910

Asn Pro Pro Pro Ser Asn Gly Gly Arg Ala Cys Gly Gly Pro Asp Ser
        915                 920                 925

Gln Ile Gln Arg Cys Asn Thr Asp Met Cys Pro Val Asp Gly Ser Trp
    930                 935                 940

Gly Ser Trp His Ser Trp Ser Gln Cys Ser Ala Ser Cys Gly Gly Gly
945                 950                 955                 960

Glu Lys Thr Arg Lys Arg Leu Cys Asp His Pro Val Pro Val Lys Gly
                965                 970                 975

Gly Arg Pro Cys Pro Gly Asp Thr Thr Gln Val Thr Arg Cys Asn Val
            980                 985                 990

Gln Ala Cys Pro Gly Gly Pro Gln Arg Ala Arg Gly Ser Val Ile Gly
        995                1000                1005

Asn Ile Asn Asp Val Glu Phe Gly Ile Ala Phe Leu Asn Ala Thr Ile
   1010                1015                1020

Thr Asp Ser Pro Asn Ser Asp Thr Arg Ile Ile Arg Ala Lys Ile Thr
1025                1030                1035                1040

Asn Val Pro Arg Ser Leu Gly Ser Ala Met Arg Lys Ile Val Ser Ile
                1045                1050                1055

Leu Asn Pro Ile Tyr Trp Thr Thr Ala Lys Glu Ile Gly Glu Ala Val
            1060                1065                1070

Asn Gly Phe Thr Leu Thr Asn Ala Val Phe Lys Arg Glu Thr Gln Val
        1075                1080                1085

Glu Phe Ala Thr Gly Glu Ile Leu Gln Met Ser His Ile Ala Arg Gly
   1090                1095                1100

Leu Asp Ser Asp Gly Ser Leu Leu Leu Asp Ile Val Val Ser Gly Tyr
1105                1110                1115                1120

Val Leu Gln Leu Gln Ser Pro Ala Glu Val Thr Val Lys Asp Tyr Thr
                1125                1130                1135

Glu Asp Tyr Ile Gln Thr Gly Pro Gly Gln Leu Tyr Ala Tyr Ser Thr
            1140                1145                1150

Arg Leu Phe Thr Ile Asp Gly Ile Ser Ile Pro Tyr Thr Trp Asn His
        1155                1160                1165
```

```
Thr Val Phe Tyr Asp Gln Ala Gln Gly Arg Met Pro Phe Leu Val Glu
   1170                1175                1180

Thr Leu His Ala Ser Ser Val Glu Ser Asp Tyr Asn Gln Ile Glu Glu
1185                1190                1195                1200

Thr Leu Gly Phe Lys Ile His Ala Ser Ile Ser Lys Gly Asp Arg Ser
               1205                1210                1215

Asn Gln Cys Pro Ser Gly Phe Thr Leu Asp Ser Val Gly Pro Phe Cys
           1220                1225                1230

Ala Asp Glu Asp Glu Cys Ala Ala Gly Asn Pro Cys Ser His Ser Cys
       1235                1240                1245

His Asn Ala Met Gly Thr Tyr Tyr Cys Ser Cys Pro Lys Gly Leu Thr
   1250                1255                1260

Ile Ala Ala Asp Gly Arg Thr Cys Gln Asp Ile Asp Glu Cys Ala Leu
1265                1270                1275                1280

Gly Arg His Thr Cys His Ala Gly Gln Asp Cys Asp Asn Thr Ile Gly
               1285                1290                1295

Ser Tyr Arg Cys Val Val Arg Cys Gly Ser Gly Phe Arg Arg Thr Ser
           1300                1305                1310

Asp Gly Leu Ser Cys Gln Asp Ile Asn Glu Cys Gln Glu Ser Ser Pro
       1315                1320                1325

Val Thr Ser Ala Val Ser Met Pro
   1330                1335
```

<210> 34
<211> 4073
<212> DNA
<213> human

<400> 34

```
actcctatag ggcggccgcg aattcggcac caggataaaa gaactgtgga tctcactgtc 60
caagttccac cttccatagc tgatgagcct acagatttcc tagtaaccaa acatgcccca 120
gcagtaatta cctgcactgc ttcgggagtt ccatttccct caattcactg gaccaaaaat 180
ggtataagac tgcttcccag gggagatggc tatagaattc tgtcctcagg agcaattgaa 240
atacttgcca cccaattaaa ccatgctgga agatacactt gtgtcgctag gaatgcggct 300
ggctctgcac atcgacacgt gacccttcat gttcatgagc ctccagtcat tcagccccaa 360
ccaagtgaac tacacgtcat tctgaacaat cctattttat taccatgtga agcaacaggg 420
acacccagtc ctttcattac ttggcaaaaa gaaggcatca atgttaacac ttcaggcaga 480
aaccatgcag ttcttcctag tggcggctta cagatctcca gagctgtccg agaggatgct 540
ggcacttaca tgtgtgtggc ccagaacccg gctggtacag ccttgggcaa aatcaagtta 600
aatgtccaag ttcctccagt cattagccct catctaaagg aatatgttat tgctgtggac 660
aagcccatca cgttatcctg tgaagcagat ggcctccctc cgcctgacat tacatggcat 720
aaagatgggc gtgcaattgt ggaatctatc cgccagcgcg tcctcagctc tggctctctg 780
caaatagcat ttgtccagcc tggtgatgct ggccattaca cgtgcatggc agccaatgta 840
gcaggatcaa gcagcacaag caccaagctc accgtccatg taccacccag gatcagaagt 900
acaaaaggac actacacggt caatgagaat tcacaagcca ttcttccatg cgtagctgat 960
ggaatcccca caccagcaat taactggaaa aaagacaatg ttcttttagc taacttgtta 1020
```

ggaaaataca ctgctgaacc atatggagaa ctcattttag aaaatgttgt gctggaggat 1080
tctggcttct atacctgtgt tgctaacaat gctgcaggtg aagatacaca cactgtcagc 1140
ctgactgtgc atgttctccc cacttttact gaacttcctg gagacgtgtc attaaataaa 1200
ggagaacagc tacgattaag ctgtaaagct actggtattc cattgcccaa attaacatgg 1260
accttcaata acaatattat tccagcccac tttgacagtg tgaatggaca cagtgaactt 1320
gttattgaaa gagtgtcaaa agaggattca ggtacttatg tgtgcaccgc agagaacagc 1380
gttggctttg tgaaggcaat tggatttgtt tatgtgaaag aacctccagt cttcaaaggt 1440
gattatcctt ctaactggat tgaaccactt ggtgggaatg caatcctgaa ttgtgaggtg 1500
aaaggagacc ccaccccaac catccagtgg aacagaaagg gagtggatat tgaaattagc 1560
cacagaatcc ggcaactggg caatggctcc ctggccatct atggcactgt taatgaagat 1620
gccggtgact atacatgtgt agctaccaat gaagctgggg tggtggagcg cagcatgagt 1680
ctgactctgc gaagtcctcc tattatcact cttgagccag tggaaactgt tattaatgct 1740
ggtggcaaaa tcatattgaa ttgtcaggca actggagagc ctcaaccaac cattacatgg 1800
tcccgtcaag ggcactctat ttcctgggat gaccgggtta acgtgttgtc caacaactca 1860
ttatatattg ctgatgctca gaaagaagat acctctgaat ttgaatgtgt tgctcgaaac 1920
ttaatgggtt ctgtccttgt cagagtgcca gtcatagtcc aggttcatgg tggattttcc 1980
cagtggtctg catggagagc ctgcagtgtc acctgtggaa aaggcatcca aaagaggagt 2040
cgtctgtgca accagcccct tccagccaat ggtgggaagc cctgccaagg ttcagatttg 2100
gaaatgcgaa actgtcaaaa taagccttgt ccagtggatg gtagctggtc ggaatggagt 2160
ctttgggaag aatgcacaag gagctgtgga cgcggcaacc aaaccaggac caggacttgc 2220
aataatccat cagttcagca tggtgggcgg ccatgtgaag ggaatgctgt ggaaataatt 2280
atgtgcaaca ttaggccttg cccagttcat ggagcatgga gcgcttggca gccttgggga 2340
acatgcagcg aaagttgtgg gaaaggtact cagacaagag caagactttg taataaccca 2400
ccaccagcgt ttggtgggtc ctactgtgat ggagcagaaa cacagatgca agtttgcaat 2460
gaaagaaatt gtccaattca tggcaagtgg gcgacttggg ccagttggag tgcctgttct 2520
gtgtcatgtg gaggaggtgc cagacagaga acaaggggct gctccgaccc tgtgccccag 2580
tatggaggaa ggaaatgcga agggagtgat gtccagagtg atttttgcaa cagtgaccct 2640
tgcccaaccc atggtaactg gagtccttgg agtggctggg gaacatgcag ccggacgtgt 2700
aacggagggc agatgcggcg gtaccgcaca tgtgataacc ctcctccctc caatggggga 2760
agagcttgtg ggggaccaga ctcccagatc cagaggtgca acactgacat gtgtcctgtg 2820
gatggaagtt ggggaagctg gcatagttgg agccagtgct ctgcctcctg tggaggaggt 2880
gaaaagactc ggaagcggct gtgcgaccat cctgtgccag ttaaaggtgg ccgtccctgt 2940
cccggagaca ctactcaggt gaccaggtgc aatgtacaag catgtccagg tgggccccag 3000
cgagccagag gaagtgttat tggaaatatt aatgatgttg aatttggaat tgctttcctt 3060
aatgccacaa taactgatag ccctaactct gatactagaa taatacgtgc caaaattacc 3120
aatgtacctc gtagtcttgg ttcagcaatg agaaagatag tttctattct aaatcccatt 3180
tattggacaa cagcaaagga aataggagaa gcagtcaatg gctttaccct caccaatgca 3240
gtcttcaaaa gagaaactca agtggaattt gcaactggag aaatcttgca gatgagtcat 3300
attgcccggg gcttggattc cgatggttct ttgctgctag atatcgttgt gagtggctat 3360
gtcctacagc ttcagtcacc tgctgaagtc actgtaaagg attacacaga ggactacatt 3420
caaacaggtc ctgggcagct gtacgcctac tcaacccggc tgttcaccat tgatggcatc 3480
agcatcccat acacatggaa ccacaccgtt ttctatgatc aggcacaggg aagaatgcct 3540
ttcttggttg aaacacttca tgcatcctct gtggaatctg actataacca gatagaagag 3600
acactgggtt ttaaaattca tgcttcaata tccaaaggag atcgcagtaa tcagtgcccc 3660
tccgggttta ccttagactc agttggacct ttttgtgctg atgaggatga atgtgcagca 3720
gggaatccct gctcccatag ctgccacaat gccatgggga cttactactg ctcctgccct 3780
aaaggcctca ccatagctgc agatggaaga acttgtcaag atattgatga gtgtgctttg 3840
ggtaggcata cctgccacgc tggtcaggac tgtgacaata cgattggatc ttatcgctgt 3900
gtggtccgtt gtggaagtgg ctttcgaaga acctctgatg ggctgagttg tcaagatatt 3960
aatgaatgtc aagaatccag ccctgtcacc agcgctgttt caatgccata ggaagtttcc 4020
attgtggatg tgaacctggg tatcagctca aaggcagaaa atgcatggat tgt 4073